

SEQUENCE LISTING

<110> Cahoon, Edgar B.  
Cahoon, Rebecca E.

<120> Enzymes Involved In Petroselinic Acid Biosynthesis

<130> BB1413 US NA

<140>

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<150> 60/169,968  
<151> 9 DECEMBER 1999

<160> 12

<170> Microsoft Office 97

<210> 1  
<211> 1344  
<212> DNA  
<213> Hedera helix

<220>

<221> unsure  
<222> (997)

<400> 1

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agagtttagct ctccaagggt tttcatggct tccactgtca actctaactc catggttctt 180  
gataatctca aaagtccgccc aaatcttcaa gtcactcaact ctagccacc caaaaagcta 240  
gaaatattca agtcccttga tgattgggtt aggaacaatg tggattca cctcaaatct 300  
gtcgagaaat ctggcaacc acaagactac ttgccggatc cggtgtcaga cggattcgag 360  
gagcaagtgc gggagtttag gaaaaaggcc aaggagattc ccgacgacta ttttggtt 420  
ttagttggag atatgatcac agaagaagca cttccaaatcat atatgtctat gctcaatagg 480  
tgtgatggta ttaaggatga gactggggct gagcccaatg cttggcaat gtggactagg 540  
gcatggactg ccgaagagaa tagacatggt gacccatctca ataagtacat ttatttgc 600  
ggaagggttg atatgaggaa aattgagaag actattcaat atctcatcg 660  
gatataatcgat cagaaaacacg cccctaccta gccttcatct acacatcctt 720  
gcaacccatca tatccatgc caacacagcc aagctggccc aacactacgg cgacaagaac 780  
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tgcgacatct tagagttct ggtggataaa tggatgtgg aaaggcttac ggggctgtcg 1080  
gacgaggggc gaaaagcgca ggaatatgtg tgtgaattgg gtcccaagat taggcgagtg 1140  
gaagagaaaag tgcaaggaa ggagaagaag aagaaagctg agcaccctgt ttcttcagc 1200  
tggattttca atcgggagtt gaagatatga acaggaagg aaggaaatgg aggagcaaata 1260  
gagtgttagta gatttctata tgcatttttatattatga atgattatta tataataata 1320  
agtgttttag ttttaagtaa aaaa 1344

<210> 2  
<211> 394  
<212> PRT  
<213> Hedera helix

<220>

<221> UNSURE  
<222> (318)

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Phe Ala Lys Ser Pro Leu Pro Val Thr Arg Val Ser Ser Pro Arg Val  
20 25 30  
  
Phe Met Ala Ser Thr Val Asn Ser Asn Ser Met Val Leu Asp Asn Leu  
35 40 45  
  
Lys Ser Pro Pro Asn Leu Gln Val Thr His Ser Met Pro Pro Gln Lys  
50 55 60  
  
Leu Glu Ile Phe Lys Ser Leu Asp Asp Trp Ala Arg Asn Asn Val Leu  
65 70 75 80  
  
Ile His Leu Lys Ser Val Glu Lys Ser Trp Gln Pro Gln Asp Tyr Leu  
85 90 95  
  
Pro Asp Pro Val Ser Asp Gly Phe Glu Glu Gln Val Arg Glu Leu Arg  
100 105 110  
  
Glu Arg Ala Lys Glu Ile Pro Asp Asp Tyr Phe Val Val Leu Val Gly  
115 120 125  
  
Asp Met Ile Thr Glu Glu Ala Leu Pro Thr Tyr Met Ser Met Leu Asn  
130 135 140  
  
Arg Cys Asp Gly Ile Lys Asp Glu Thr Gly Ala Glu Pro Ser Ala Trp  
145 150 155 160  
  
Ala Met Trp Thr Arg Ala Trp Thr Ala Glu Glu Asn Arg His Gly Asp  
165 170 175  
  
Leu Leu Asn Lys Tyr Leu Tyr Leu Ser Gly Arg Val Asp Met Arg Lys  
180 185 190  
  
Ile Glu Lys Thr Ile Gln Tyr Leu Ile Gly Ser Gly Met Asp Ile Lys  
195 200 205  
  
Ser Glu Asn Ser Pro Tyr Leu Gly Phe Ile Tyr Thr Ser Phe Gln Glu  
210 215 220  
  
Arg Ala Thr Phe Ile Ser His Ala Asn Thr Ala Lys Leu Ala Gln His  
225 230 235 240  
  
Tyr Gly Asp Lys Asn Leu Ala His Ile Cys Gly Ser Ile Ala Ser Asp  
245 250 255  
  
Glu Lys Arg His Ala Thr Ala Tyr Thr Lys Ile Val Glu Lys Leu Ala  
260 265 270  
  
Glu Ile Asp Pro Asp Thr Thr Val Ile Ala Phe Ala Asp Met Met Arg  
275 280 285  
  
Lys Lys Ile Thr Met Pro Ala His Leu Met Tyr Asp Gly Ser Asp Glu  
290 295 300

Leu Leu Phe Lys His Phe Thr Ala Val Ala Gln Arg Val Xaa Val Tyr  
305 310 315 320

Ser Ala Leu Asp Tyr Cys Asp Ile Leu Glu Phe Leu Val Asp Lys Trp  
325 330 335

Asn Val Glu Arg Leu Thr Gly Leu Ser Asp Glu Gly Arg Lys Ala Gln  
340 345 350

Glu Tyr Val Cys Glu Leu Gly Pro Lys Ile Arg Arg Val Glu Glu Lys  
355 360 365

Val Gln Gly Lys Glu Lys Lys Lys Ala Glu His Pro Val Ser Phe  
370 375 380

Ser Trp Ile Phe Asn Arg Glu Leu Lys Ile  
385 390

<210> 3

<211> 445

<212> DNA

<213> Hedera helix

<400> 3

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catcgatttc cttcacctctt atcgcaagct ccctcaagca aaaccaggga cttgccaaga 180  
gttcaatttc actctctgttc aatggaaat cttccgttc acttaggttg ctgtcggcac 240  
cacttcgctt cagagtgtca tgcgcagcga aaccagcgcac agtggacaag gtgtgtgaga 300  
ttgtgcgaaaa acaactggcg ctgcccgtga ttctgcaagt cactggagag tcaaaaattcg 360  
cagcgcttgg ggctgattctt ctcgacacgg ttgagattgt gatggacta aaggaggaat 420  
tcggaatcaa gcgtggaaaa aagaa 445

<210> 4

<211> 114

<212> PRT

<213> Hedera helix

<400> 4

Met Ala Ser Val Thr Ala Ser Ser Ile Ser Phe Thr Ser Ile Ala Ser  
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Ser Leu Lys Gln Asn Gln Gly Leu Ala Lys Ser Ser Ile Ser Leu Ser  
20 25 30

Val Asn Gly Lys Ser Phe Arg Ser Leu Arg Leu Leu Ser Ala Pro Leu  
35 40 45

Arg Phe Arg Val Ser Cys Ala Ala Lys Pro Ala Thr Val Asp Lys Val  
50 55 60

Cys Glu Ile Val Arg Lys Gln Leu Ala Leu Pro Leu Ile Leu Gln Val  
65 70 75 80

Thr Gly Glu Ser Lys Phe Ala Ala Leu Gly Ala Asp Ser Leu Asp Thr  
85 90 95

Val Glu Ile Val Met Gly Leu Lys Glu Glu Phe Gly Ile Lys Arg Gly  
100 105 110

Lys Lys  
 114

<210> 5  
 <211> 920  
 <212> DNA  
 <213> Hedera helix

<400> 5  
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 catcgatttc ctccacctctt atcgcaagct ccctcaagca aaaccaggga cttgccaaga 180  
 gttcaatttc actctctgtc aatggaaat cttccgttc acttaggttgcgtcggcac 240  
 cacttcgctt cagagtgtca tgccgacgcga aaccagcgcac agtggacaag gtgtgtgaga 300  
 ttgtgcggaa acaactggcg ctgcccgtt attctgcagt cactggagag tcaaaaattcg 360  
 cagcgcttgg ggctgattctt ctcgacacgg ttgagattgt gatggacta gaggagaaat 420  
 tcggaatcag cggtggaaagaa gaaagtgcac agaccattgc cactgttcaa gatgcagcgg 480  
 acctgattga gaagcttggttt gagaaaaagg agtggacaag ccggggtagaaattctgcaa 540  
 aatacggtta ttaaggacag ttacttttattt aggatggttc atcaagatct tcattaccct 600  
 acatttattt gtatgctcctt catgaagccg caaaagttagt agtggtgatg aaatttaccc 660  
 cgagtcttcg ccttaatttat caaagtggaa gagccagaaa aagaggctat gctatctc 720  
 atctcggttat gttttatattt cttgtcgac ttctgggtttt agtttttttttttatactaa 780  
 acatgatattt agtcttggttt aaaagttctt caaaaaaaaata tatcttggttg ttgagactga 840  
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<210> 6  
 <211> 137  
 <212> PRT  
 <213> Hedera helix

<400> 6  
 Met Ala Ser Val Thr Ala Ser Ser Ile Ser Phe Thr Ser Ile Ala Ser  
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Ser Leu Lys Gln Asn Gln Gly Leu Ala Lys Ser Ser Ile Ser Leu Ser  
 20 25 30

Val Asn Gly Lys Ser Phe Arg Ser Leu Arg Leu Leu Ser Ala Pro Leu  
 35 40 45

Arg Phe Arg Val Ser Cys Ala Ala Lys Pro Ala Thr Val Asp Lys Val  
 50 55 60

Cys Glu Ile Val Arg Lys Gln Leu Ala Leu Pro Ala Asp Ser Ala Val  
 65 70 75 80

Thr Gly Glu Ser Lys Phe Ala Ala Leu Gly Ala Asp Ser Leu Asp Thr  
 85 90 95

Val Glu Ile Val Met Gly Leu Glu Glu Glu Phe Gly Ile Ser Val Glu  
 100 105 110

Glu Glu Ser Ala Gln Thr Ile Ala Thr Val Gln Asp Ala Ala Asp Leu  
 115 120 125

Ile Glu Lys Leu Val Glu Lys Lys Glu  
 130 135

<210> 7  
 <211> 385  
 <212> PRT  
 <213> *Coriandrum sativum*

<400> 7  
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Asn Met Phe Thr Arg Ile Ala Pro Pro Gln Ala Gly Arg Val Arg Ser  
     20                 25                         30

Lys Val Ser Met Ala Ser Thr Leu His Ala Ser Pro Leu Val Phe Asp  
     35                 40                         45

Lys Leu Lys Ala Gly Arg Pro Glu Val Asp Glu Leu Phe Asn Ser Leu  
     50                 55                         60

Glu Gly Trp Ala Arg Asp Asn Ile Leu Val His Leu Lys Ser Val Glu  
     65                 70                         75                 80

Asn Ser Trp Gln Pro Gln Asp Tyr Leu Pro Asp Pro Thr Ser Asp Ala  
     85                 90                         95

Phe Glu Asp Gln Val Lys Glu Met Arg Glu Arg Ala Lys Asp Ile Pro  
     100                 105                         110

Asp Glu Tyr Phe Val Val Leu Val Gly Asp Met Ile Thr Glu Glu Ala  
     115                 120                         125

Leu Pro Thr Tyr Met Ser Met Leu Asn Arg Cys Asp Gly Ile Lys Asp  
     130                 135                         140

Asp Thr Gly Ala Gln Pro Thr Ser Trp Ala Thr Trp Thr Arg Ala Trp  
     145                 150                         155                 160

Thr Ala Glu Glu Asn Arg His Gly Asp Leu Leu Asn Lys Tyr Leu Tyr  
     165                 170                         175

Leu Ser Gly Arg Val Asp Met Arg Met Ile Glu Lys Thr Ile Gln Tyr  
     180                 185                         190

Leu Ile Gly Ser Gly Met Asp Thr Lys Thr Glu Asn Cys Pro Tyr Met  
     195                 200                         205

Gly Phe Ile Tyr Thr Ser Phe Gln Glu Arg Ala Thr Phe Ile Ser His  
     210                 215                         220

Ala Asn Thr Ala Lys Leu Ala Gln His Tyr Gly Asp Lys Asn Leu Ala  
     225                 230                         235                 240

Gln Val Cys Gly Asn Ile Ala Ser Asp Glu Lys Arg His Ala Thr Ala  
     245                 250                         255

Tyr Thr Lys Ile Val Glu Lys Leu Ala Glu Ile Asp Pro Asp Thr Thr  
     260                 265                         270

Val Ile Ala Phe Ser Asp Met Met Arg Lys Lys Ile Gln Met Pro Ala  
     275                 280                         285

His Ala Met Tyr Asp Gly Ser Asp Asp Met Leu Phe Lys His Phe Thr  
 290 295 300  
 Ala Val Ala Gln Gln Ile Gly Val Tyr Ser Ala Trp Asp Tyr Cys Asp  
 305 310 315 320  
 Ile Ile Asp Phe Leu Val Asp Lys Trp Asn Val Ala Lys Met Thr Gly  
 325 330 335  
 Leu Ser Gly Glu Gly Arg Lys Ala Gln Glu Tyr Val Cys Ser Leu Ala  
 340 345 350  
 Ala Lys Ile Arg Arg Val Glu Glu Lys Val Gln Gly Lys Glu Lys Lys  
 355 360 365  
 Ala Val Leu Pro Val Ala Phe Ser Trp Ile Phe Asn Arg Gln Ile Ile  
 370 375 380  
 Ile  
 385  
 <210> 8  
 <211> 137  
 <212> PRT  
 <213> Coriandrum sativum  
 <400> 8  
 Met Ala Ala Phe Thr Ala Ser Ser Val Ser Phe Thr Pro Leu Ser Ile  
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 Ser Leu Asn Gln Thr Lys Gly Phe Ala Arg Gly Ser Val Ser Ile Pro  
 20 25 30  
 Ala Lys Ala Lys Ser Phe Gly Ala Leu Thr Leu Arg Asn Ala Pro Leu  
 35 40 45  
 Arg Phe Arg Val Ser Cys Ala Ala Lys Pro Glu Thr Val Glu Lys Val  
 50 55 60  
 Cys Glu Ile Val Lys Lys Gln Leu Ala Leu Pro Pro Thr Thr Glu Val  
 65 70 75 80  
 Ser Gly Asp Ser Lys Phe Ala Ala Leu Gly Ala Asp Ser Leu Asp Thr  
 85 90 95  
 Val Glu Ile Val Met Gly Leu Glu Glu Glu Phe Gly Ile Ser Val Glu  
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 115 120 125  
 Ile Glu Lys Leu Cys Glu Lys Lys Glu  
 130 135  
 <210> 9  
 <211> 1381  
 <212> DNA  
 <213> Hedera helix

<400> 9  
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aagaagaacc accctgctgc gtttgcataag tcaccattac cagtgaccag agttagctct 180  
ccaagggtt tcatggcttc cactgtcaac tctaactcca tggttcttga taatctcaa 240  
agtcctccaa atcttcaagt cactcactct atgccacccc aaaagctaga aatattcaag 300  
tcccttgatg attgggctag gaacaatgtg ttgattcacc tcaaatactgt cgagaaatct 360  
tggcaaccac aagactactt gcccgatccg gtgtcagacg gattcgagga gcaagtgcgg 420  
gagttgaggg aaaggccaa ggagattccc gacgactatt ttgtgggtt agttggagat 480  
atgatcacag aagaagact tccaaacatat atgtctatgc tcaataggtg tgatgttatt 540  
aaggatgaga ctggggctga gcccagtgtc tgggcaatgt ggactagggc atggactgcc 600  
gaagagaata gacatggtga ctttctcaat aagtacctt atttgtctgg aagggttcat 660  
atgagggaaa ttgagaagac tattcaatat ctcatcggt caggaatggc tatcaagtca 720  
aaaaacagcc cctacctagg cttcatctac acatccttcc aagagagagc aaccttcata 780  
tcccatgcca acacagccaa gctggccaa cactacggcg acaagaacct cgctcacatc 840  
tgcggctcca tgcctccga cgagaagcgc 900  
aagctcgctg agatcgaccc cgacacacaaca gtaattgtt ttgcagat 960  
aaaataacaa tgccagcgc 1020  
ttcacggcgg ttgctcagag agtgggggtt tattctcg 1080  
gagtttctgg tggataaaatg gaatgtggaa aggcttacgg 1140  
aaagcgcagg aatatgtgtg tgaattgggt cccaagatta 1200  
caygggaagg agaagaagaa gaaagctgag caccctgttt 1260  
cgggagttga agatatgaac aggaaggaa gggaaatggag 1320  
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<210> 10  
<211> 394  
<212> PRT  
<213> Hedera helix

<400> 10

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20 25 30

Phe Met Ala Ser Thr Val Asn Ser Asn Ser Met Val Leu Asp Asn Leu  
35 40 45

Lys Ser Pro Pro Asn Leu Gln Val Thr His Ser Met Pro Pro Gln Lys  
50 55 60

Leu Glu Ile Phe Lys Ser Leu Asp Asp Trp Ala Arg Asn Asn Val Leu  
65 70 75 80

Ile His Leu Lys Ser Val Glu Lys Ser Trp Gln Pro Gln Asp Tyr Leu  
85 90 95

Pro Asp Pro Val Ser Asp Gly Phe Glu Glu Gln Val Arg Glu Leu Arg  
100 105 110

Glu Arg Ala Lys Glu Ile Pro Asp Asp Tyr Phe Val Val Leu Val Gly  
115 120 125

Arg Cys Asp Gly Ile Lys Asp Glu Thr Gly Ala Glu Pro Ser Ala Trp  
145 150 155 160

Ala Met Trp Thr Arg Ala Trp Thr Ala Glu Glu Asn Arg His Gly Asp  
165 170 175

Leu Leu Asn Lys Tyr Leu Tyr Leu Ser Gly Arg Val Asp Met Arg Lys  
180 185 190

Ile Glu Lys Thr Ile Gln Tyr Leu Ile Gly Ser Gly Met Asp Ile Lys  
195 200 205

Ser Glu Asn Ser Pro Tyr Leu Gly Phe Ile Tyr Thr Ser Phe Gln Glu  
210 215 220

Arg Ala Thr Phe Ile Ser His Ala Asn Thr Ala Lys Leu Ala Gln His  
225 230 235 240

Tyr Gly Asp Lys Asn Leu Ala His Ile Cys Gly Ser Ile Ala Ser Asp  
245 250 255

Glu Lys Arg His Ala Thr Ala Tyr Thr Lys Ile Val Glu Lys Leu Ala  
260 265 270

Glu Ile Asp Pro Asp Thr Thr Val Ile Ala Phe Ala Asp Met Met Arg  
275 280 285

Lys Lys Ile Thr Met Pro Ala His Leu Met Tyr Asp Gly Ser Asp Glu  
290 295 300

Leu Leu Phe Lys His Phe Thr Ala Val Ala Gln Arg Val Gly Val Tyr  
305 310 315 320

Ser Ala Leu Asp Tyr Cys Asp Ile Leu Glu Phe Leu Val Asp Lys Trp  
325 330 335

Asn Val Glu Arg Leu Thr Gly Leu Ser Asp Glu Gly Arg Lys Ala Gln  
340 345 350

Glu Tyr Val Cys Glu Leu Gly Pro Lys Ile Arg Arg Val Glu Glu Lys  
355 360 365

Val Gln Gly Lys Glu Lys Lys Lys Ala Glu His Pro Val Ser Phe  
370 375 380

Ser Trp Ile Phe Asn Arg Glu Leu Lys Ile  
385 390

<210> 11  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> PCR primer

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<210> 12  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> PCR primer

<400> 12  
atgagctccc ttccctgttca tatcttc

27